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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/758,003

DATE: 07/30/2001
TIME: 12:09:42

Input Set : N:\Crf3\RULE60\09758003.txt
Output Set: N:\CRF3\07302001\I758003.raw

SEQUENCE LISTING

ENI EHRD

- 2 (1) GENERAL INFORMATION:
 3 (i) APPLICANT: BALCHWAL, VIJAY R
 4 HUANG, JIANNING
 5 HOU, HAILING
 6 SHEDDEL, DAVID V
 7 (ii) TITLE OF INVENTION: FIP: NOVEL HUMAN PROTEIN INVOLVED IN
 8 TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
 9 ASSAYS
 10 (iii) NUMBER OF SEQUENCES: 2
 11 (iv) CORRESPONDENCE ADDRESS:
 12 (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 13 (B) STREET: 19 DENISE DRIVE
 14 (C) CITY: BILLERICA
 15 (D) STATE: CALIFORNIA
 16 (E) COUNTRY: USA
 17 (F) ZIP: 94010
 18 (v) COMPUTER READABLE FORM:
 19 (A) MEDIUM TYPE: Floppy disk
 20 (B) COMPUTER: IBM PC compatible
 21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 23 (vi) CURRENT APPLICATION DATA:
 24 (A) APPLICATION NUMBER: US/09/758,003
 25 (B) FILING DATE: 09-Jan-2001
 26 (C) CLASSIFICATION:
 27 (vii) PRIOR APPLICATION DATA:
 28 (A) APPLICATION NUMBER: 09/133,118
 29 (B) FILING DATE:
 30 (viii) ATTORNEY/AGENT INFORMATION:
 31 (A) NAME: OPMAN, RICHARD A.
 32 (B) REGISTRATION NUMBER: 36,627
 33 (C) REFERENCE/DOCKET NUMBER: T95-006-1
 34 (ix) TELECOMMUNICATION INFORMATION:
 35 (A) TELEPHONE: (650) 343-4541
 36 (B) TELEFAX: (650) 343-4342
 37 (2) INFORMATION FOR SEQ ID NO: 1:
 38 (i) SEQUENCE CHARACTERISTICS:
 39 (A) LENGTH: 201 base pairs
 40 (B) TYPE: nucleic acid
 41 (C) STRANDEDNESS: double
 42 (D) TOPOLOGY: linear
 43 (ii) MOLECULE TYPE: cDNA
 44 (ix) FEATURE:
 45 (A) NAME/KEY: CDS
 46 (B) LOCATION: 1...513
 47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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52 ATG CAA CCA GAT ATG TCC TTG AAT GTC ATT AAG ATG AAA TCC AAT GAC	43
53 Met Gln Pro Asp Met Ile Leu Asn Val Ile Lys Met Lys Ser Ser Asp	
54 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100	
55 TTC CTG GAG ACT TCA CAA CTC GAC AGC GAA GCG TTT CGG AAG GTG TCT	96
56 Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser	
57 21 26 31 36 41 46 51 56 61 66 71 76 81 86 91 96 101	
58 CTG TGT TTC CAC AGA AAC CAG GGA CTC ATG ATG ATG AAA AGA GTG TAC	144
59 Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr	
60 31 36 41 46 51 56 61 66 71 76 81 86 91 96 101	
61 AAG GGG CCT AAA TCC ATT GAG CAC AAC GAG GAA CTC TTG TAC GAG GCG	149
62 Lys Gly Pro Asn Lys Ile Glu His Asn Glu Ala Leu Leu Glu Asp	
63 58 63 68 73 78 83 88 93 98 103 108 113 118 123 128 133 138 143	
64 AAG ATG ATG AAC AGA CTG AGA CAC AGC CGG GTG GPG AAG TTC CTG GGC	240
65 Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly	
66 61 66 71 76 81 86 91 96 101 106 111 116 121 126 131 136 141	
67 GTC ATC ATA GAG GAA GGG AAG TAC TCC CTC GTG ATG GAG TAC ATG GAG	288
68 Val Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu	
69 74 79 84 89 94 99 104 109 114 119 124 129 134 139 144 149 154	
70 AAG GGC AAC CTG ATG CAC GTG CTG AAA GCC GAG ATG AGT ACT CCG CTT	336
71 Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu	
72 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180	
73 TCT GTA AAA CGA AGG ATA ATT TTG GAA ATC ATT GAA GGA ATG TGC TAC	384
74 Ser Val Lys Glu Arg Ile Ile Leu Glu Ile Glu Gly Met Cys Tyr	
75 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190	
76 TTA CAT GGA AAA GGC GTG ATA CAC AAG GAC CTG AAG CCT GAA AAT ATC	432
77 Leu His Glu Lys Glu Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile	
78 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205	
79 CTT GTT GAT AAT GAC TTC CAC ATT AAG ATC GCA GAC CTC GGC CTT GGC	480
80 Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala	
81 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225	
82 TCC TTT AAG ATG TGG AGC AAA CTG AAT AAT GAA GAG CAC AAT GAG CTG	528
83 Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu	
84 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245	
85 AGG GAA GTG GAC GGC ACC GCT AAG AAG AAT GGC GGC ACC CTC TAC TAC	576
86 Arg Glu Val Asp Glu Thr Ala Lys Lys Asn Glu Gly Thr Leu Tyr Tyr	
87 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260	
88 ATG GCG CCC GAG CAC CTG AAT GAC GTC AAC GCA AAG CCC ACA GAG AAG	624
89 Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys	
90 190 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275	
91 TCG GAT GTG TAC AGC TTT GCT GTA CTC CTC TGG GCG ATA TTT GCA AAT	672
92 Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn	
93 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290	
94 AAG GAG CCA TAT GAA AAT GCT ATC TGT GAG CAG CAG TTG ATA ATG TGG	720
95 Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys	
96 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305	
97 ATA AAA TCT GGG AAC AGG CCA GAT GTG GAT GAC ATC ACT GAG TAC TGG	768
98 Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys	
99 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325	
100 CCA AGA GAA ATT ATC AGT CTC ATG AAG CTC TGC TGG GAA GCG AAT CCG	816

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101	Pro	Arg	Glu	Ile	Ile	Ser	Leu	Met	Lys	Leu	Cys	Trp	Glu	Ala	Asn	Pro	
102																	
	261							265								270	
103	GAA	GCT	CGG	CTG	ACA	TTT	TCT	GCT	ATP	GAA	GAA	AAA	TTT	AGG	CCT	TTT	
104	Glu	Gln	Gly	Gly	Asn												364
105																	
	275							280								285	
106	TAT	TTA	AGT	CAA	TTA	GAA	AAA	AGT	GTA	GAA	GAG	GAC	CTG	AAG	AGT	TTA	
107	Tyr	Leu	Ser	Gln	Leu	Glu	Glu	Ser	Val	Glu	Glu	Asp	Val	Lys	Ser	Leu	
108																	312
	290							295								300	
109	AAG	AAA	GAG	TAT	TCA	ARC	GAA	ATP	GCA	CTT	GTC	AAG	AGA	ATC	GAC	TTT	
110	Lys	Lys	Gln	Tyr	Ser	Asn	Gln	Ala	Val	Val	Val	Lys	Asn	Met	Gln	Ter	
111																320	
	305							310								325	
112	CPT	CAA	CPT	GAT	TGT	GTG	GCA	STA	CCT	TCA	AGC	GGG	TCA	ATC	TCA	GCC	
113	Leu	Leu	Leu	Asn	Cys	Val	Ala	Val	Pro	Ser	Ser	Arg	Ser	Asn	Ser	Ala	
114																330	
	325							330								335	
115	ACA	GAA	CAG	CCT	GGT	ATA	CTG	CAC	AGT	TCC	CAG	GGA	CTT	GGG	ATG	GGT	
116	Thr	Glu	Gln	Pro	Gly	Ser	Leu	His	Ser	Ser	Gln	Gly	Leu	Gly	Met	Gly	
117																340	
	340							345								350	
118	CCT	GTG	GAG	GAG	TCC	TTT	GCT	CCT	TCC	CTG	GAG	CAC	CCA	CAA	GAA	1104	
119	Pro	Val	Glu	Glu	Ser	Tyr	Phe	Ala	Pro	Ser	Leu	Glu	His	Pro	Gln	Glu	
120																355	
	355							360								365	
121	GAG	AAT	GAG	CCC	AGC	CTG	CAG	AGT	AAA	CTC	CAA	GAC	GAA	GCC	AAC	TAC	
122	Glu	Asn	Glu	Glu	Pro	Ser	Leu	Ser	Lys	Leu	Gln	Asp	Glu	Ala	Asn	Tyr	
123																370	
	370							375								380	
124	CAT	CTT	TAT	GGC	AGC	CGC	ATG	GAC	AGG	CAG	AAA	CAG	CAC	CCC	AGA	1200	
125	His	Leu	Tyr	Gly	Ser	Arg	Met	Asp	Arg	Gln	Tyr	Lys	Gln	Gln	Pro	Arg	
126																385	
	385							390								395	
127	CAG	AAT	GTG	GCT	TAC	AAC	AGA	GAG	GAA	AGG	AGA	GCG	AGG	GTC	TCC	1248	
128	Gln	Asn	Val	Ala	Tyr	Asn	Arg	Glu	Glu	Glu	Glu	Arg	Arg	Arg	Arg	Val	
129																405	
	405							410								415	
130	CAT	GAC	CCT	TTT	GCA	CAG	CAA	AGA	CCT	TAC	GAG	AAT	TTT	CAG	AAT	ACA	
131	His	Asp	Pro	Phe	Ala	Gln	Gln	Arg	Pro	Tyr	Glu	Asn	Phe	Gln	Asn	Thr	
132																420	
	420							425								430	
133	GAG	GGA	AAA	GGC	ACT	GTT	TAT	AGT	GCA	GGC	AGT	CAT	GCT	AAT	GCA	1344	
134	Glu	Gly	Lys	Gly	Tyr	Val	Tyr	Ser	Ser	Ala	Ala	Ser	His	Gly	Asn	Ala	
135																435	
	435							440								445	
136	GTG	CAC	CAG	CCC	TCA	GGG	CTC	ACC	AGC	CAA	CCT	GAA	GTA	CTG	TAT	CAG	
137	Val	His	Gln	Pro	Ser	Gly	Leu	Thr	Ser	Gln	Pro	Gln	Val	Leu	Tyr	Gln	
138																450	
	450							455								460	
139	AAC	AAT	GGA	TTA	TAT	AGC	TCA	CAT	GGC	TTT	GGG	ACA	AGA	CCA	CTG	GAT	
140	Asn	Asn	Gly	Leu	Tyr	Ser	Ser	His	Gly	Phe	Gly	Thr	Arg	Pro	Leu	Asp	
141																465	
	465							470								480	
142	CCA	GGA	ACA	GCA	GGT	GGC	AGA	GTT	TGG	TAC	AGG	CCA	ATT	CCA	AGT	CAT	
143	Pro	Gly	Thr	Ala	Gly	Pro	Arg	Val	Trp	Tyr	Arg	Pro	Ile	Pro	Ser	His	
144																485	
	485							490								495	
145	ATG	CCT	AGT	CTG	CAT	AAT	ATC	CCA	GTC	GCT	GAG	ACC	AAC	TAT	CTA	GGA	
146	Met	Pro	Ser	Leu	His	Asn	Ile	Pro	Val	Pro	Glu	Thr	Asn	Tyr	Leu	Gly	
147																500	
	500							505								510	
148	AAT	ACA	CUC	ACC	ATG	CCA	TTC	AGC	TCC	TTG	CCA	CCA	ACA	GAT	GAA	TCT	
149	Asn	Thr	Pro	Thr	Met	Pro	Phe	Ser	Ser	Leu	Pro	Pro	Thr	Asp	Glu	Ser	

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150	915	920	925	
151	ATA AAA TAT ACC ATA TAC AAT AGT ATG GAG ATT CAG ATT GGA GCC TAC			1632
152	Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr			
153	530 535 540			
154	ATG TAT ATG GAG ATT GAG AGG ATG TAA TCA CTA CTA GAT AGG ACA			1680
155	Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr			
156	545 550 555 560			
157	AAT ATG AAC TTC AAA GAA GAG CCA CCT GCT AAG TAC CAA GGT ATG TTT			1728
158	Asn Thr Asn Ile Lys Glu Glu Pro Ala Ala Lys Tyr Glu Ala Ile Pro			
159	565 570 575			
160	GAT AAT ACC ACT ATG AGG GAT AAA CAT CTG GAC CCA ATC AGG GAA			1776
161	Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu			
162	580 585 590			
163	AAT CTG GGA AAG AAC TGG AAA AAC TGT GGT AAA CGG GGC TTC ACA			1824
164	Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr			
165	595 600 605			
166	CAG TCT CAG ATT GAT GAA ATT GAT GAT GAG TAT GAG CGA GAT GGA CTG			1872
167	Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu			
168	610 615 620			
169	AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC			1920
170	Lys Glu Lys Val Tyr Glu Met Leu Gln Lys Trp Val Met Arg Glu Gly			
171	615 630 635 640			
172	ATA AAG GGA GCC ACG CTG GGG AAG CTG GCC CAG GGG CTC CAC CAG TGT			1968
173	Ile Lys Glu Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys			
174	645 650 655			
175	TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC			2013
176	Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn			
177	660 665 670			
178	TAA			2016

180 (i) INFORMATION FOR SEQ ID NO: 2:

181 (i) SEQUENCE CHARACTERISTICS:

182 (A) LENGTH: 671 amino acids

183 (B) TYPE: amino acid

184 (C) TOPOLOGY: linear

185 (ii) MOLECULE TYPE: protein

186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

187 Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp

188 1 5 10 15

189 Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Glu Lys Val Ser

190 20 25 30

191 Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr

192 35 40 45

193 Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Ala

194 50 55 60

195 Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly

196 65 70 75 80

197 Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu

198 85 90 95

199 Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu

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200	100	105	110	
201	Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Pro Asn Gly Met Cys Tyr			
202	115	120	125	
203	Leu His Gly Lys Gly Val Ile Ile Lys Asp Leu Lys Pro Glu Asn Ile			
204	130	135	140	
205	Ile Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala			
206	145	150	155	160
207	Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu			
208	165	170	175	
209	Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr			
210	180	185	190	
211	Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys			
212	195	200	205	
213	Ser Asp Val Tyr Ser Phe Ala Val Val Ile Trp Ala Ile Phe Ala Asn			
214	210	215	220	
215	Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys			
216	225	230	235	240
217	Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys			
218	245	250	255	
219	Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro			
220	260	265	270	
221	Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe			
222	275	280	285	
223	Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu			
224	290	295	300	
225	Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser			
226	305	310	315	320
227	Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala			
228	325	330	335	
229	Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly			
230	340	345	350	
231	Pro Val Glu Gln Ser Trp Phe Ala Pro Ser Leu Gln His Pro Gln Gln			
232	355	360	365	
233	Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr			
234	370	375	380	
235	His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg			
236	385	390	395	400
237	Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser			
238	405	410	415	
239	His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr			
240	420	425	430	
241	Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala			
242	435	440	445	
243	Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln			
244	450	455	460	
245	Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp			
246	465	470	475	480
247	Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His			
248	485	490	495	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09758003.txt

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L:24 M:220 C: Keyword misspelled or invalid format, [{(A)} APPLICATION NUMBER:]
L:25 M:220 C: Keyword misspelled or invalid format, [{(B)} FILING DATE:]